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RAW SEQUENCE LISTING   DATE: 11/14/2001
PATENT APPLICATION: US/09/830,706   TIME: 14:12:30

Input Set : **A:\55871965.app**
Output Set: **N:\CRF3\11142001\I830706.raw**

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  4 <110> APPLICANT: TOJI, SHINGO
  5          YANO, MINORU
  6          TAMAI, KATSUYUKI
  8 <120> TITLE OF INVENTION: THIOREDOXIN REDUCTASE II
 10 <130> FILE REFERENCE: 55865-71965
 12 <140> CURRENT APPLICATION NUMBER: 09/830,706
 13 <141> CURRENT FILING DATE: 2001-04-27
 15 <150> PRIOR APPLICATION NUMBER: PCT/JP99/05983
 16 <151> PRIOR FILING DATE: 1999-10-28
 18 <150> PRIOR APPLICATION NUMBER: JP 1998-310422
 19 <151> PRIOR FILING DATE: 1998-10-30
 21 <160> NUMBER OF SEQ ID NOS: 38
 23 <170> SOFTWARE: PatentIn Ver. 2.1
 25 <210> SEQ ID NO: 1
 26 <211> LENGTH: 1959
 27 <212> TYPE: DNA
 28 <213> ORGANISM: Homo sapiens
 30 <220> FEATURE:
 31 <221> NAME/KEY: CDS
 32 <222> LOCATION: (10)..(1572)
 34 <220> FEATURE:
 35 <221> NAME/KEY: MOD_RES
 36 <222> LOCATION: (520)
 37 <223> OTHER INFORMATION: Selenocysteine
 39 <400> SEQUENCE: 1
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 41           Met Ala Val Ala Leu Arg Gly Leu Gly Gly Arg Phe Arg Trp
 42            1               5                  10
 44 cgg acg cag gcc gtg gcg ggc ggg gtg cgg ggc gcg gcg cgg ggc gca      99
 45 Arg Thr Gln Ala Val Ala Gly Gly Val Arg Gly Ala Ala Arg Gly Ala
 46  15                  20                  25                  30
 48 gca gca ggt cag cgg gac tat gat ctc ctg gtg gtc ggc ggg gga tct     147
 49 Ala Ala Gly Gln Arg Asp Tyr Asp Leu Leu Val Val Gly Gly Gly Ser
 50                  35                  40                  45
 52 ggt ggc ctg gct tgt gcc aag gag gcc gcc cag ctg gga agg aag gtg     195
 53 Gly Gly Leu Ala Cys Ala Lys Glu Ala Ala Gln Leu Gly Arg Lys Val
 54                  50                  55                  60
 56 gcc gtg gtg gac tac gtg gaa cct tct ccc caa ggc acc cgg tgg ggc     243
 57 Ala Val Val Asp Tyr Val Glu Pro Ser Pro Gln Gly Thr Arg Trp Gly
 58                  65                  70                  75
 60 ctc ggc ggc acc tgc gtc aac gtg ggc tgc atc ccc aag aag ctg atg     291
 61 Leu Gly Gly Thr Cys Val Asn Val Gly Cys Ile Pro Lys Lys Leu Met
 62       80                  85                  90
 64 cac cag gcg gca ctg ctg gga ggc ctg atc caa gat gcc ccc aac tat     339
 65 His Gln Ala Ala Leu Leu Gly Gly Leu Ile Gln Asp Ala Pro Asn Tyr
 66  95                  100                 105                 110
 68 ggc tgg gag gtg gcc cag ccc gtg ccg cat gac tgg agg aag atg gca     387
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 69 Gly Trp Glu Val Ala Gln Pro Val Pro His Asp Trp Arg Lys Met Ala
 70                 115                 120                 125
 72 gaa gct gtt caa aat cac gtg aaa tcc ttg aac tgg ggc cac cgt gtc   435
 73 Glu Ala Val Gln Asn His Val Lys Ser Leu Asn Trp Gly His Arg Val
 74                 130                 135                 140
 76 cag ctt cag gac aga aaa gtc aag tac ttt aac atc aaa gcc agc ttt   483
 77 Gln Leu Gln Asp Arg Lys Val Lys Tyr Phe Asn Ile Lys Ala Ser Phe
 78             145                 150                 155
 80 gtt gac gag cac acg gtt tgc ggc gtt gcc aaa ggt ggg aaa gag att   531
 81 Val Asp Glu His Thr Val Cys Gly Val Ala Lys Gly Gly Lys Glu Ile
 82         160                 165                 170
 84 ctg ctg tca gcc gat cac atc atc att gct act gga ggg cgg ccg aga   579
 85 Leu Leu Ser Ala Asp His Ile Ile Ile Ala Thr Gly Gly Arg Pro Arg
 86 175                 180                 185                 190
 88 tac ccc acg cac atc gaa ggt gcc ttg gaa tat gga atc aca agt gat   627
 89 Tyr Pro Thr His Ile Glu Gly Ala Leu Glu Tyr Gly Ile Thr Ser Asp
 90                 195                 200                 205
 92 gac atc ttc tgg ctg aag gaa tcc cct gga aaa acg ttg gtg gtc ggg   675
 93 Asp Ile Phe Trp Leu Lys Glu Ser Pro Gly Lys Thr Leu Val Val Gly
 94                 210                 215                 220
 96 gcc agc tat gtg gcc ctg gag tgt gct ggc ttc ctc acc ggg att ggg   723
 97 Ala Ser Tyr Val Ala Leu Glu Cys Ala Gly Phe Leu Thr Gly Ile Gly
 98         225                 230                 235
100 ctg gac acc acc atc atg atg cgc agc atc ccc ctc cgc ggc ttc gac   771
101 Leu Asp Thr Thr Ile Met Met Arg Ser Ile Pro Leu Arg Gly Phe Asp
102         240                 245                 250
104 cag caa atg tcc tcc atg gtc ata gag cac atg gca tct cat ggc acc   819
105 Gln Gln Met Ser Ser Met Val Ile Glu His Met Ala Ser His Gly Thr
106 255                 260                 265                 270
108 cgg ttc ctg agg ggc tgt gcc ccc tcg cgg gtc agg agg ctc cct gat   867
109 Arg Phe Leu Arg Gly Cys Ala Pro Ser Arg Val Arg Arg Leu Pro Asp
110                 275                 280                 285
112 ggc cag ctg cag gtc acc tgg gag gac agc acc acc ggc aag gag gac   915
113 Gly Gln Leu Gln Val Thr Trp Glu Asp Ser Thr Thr Gly Lys Glu Asp
114                 290                 295                 300
116 acg ggc acc ttt gac acc gtc ctg tgg gcc ata ggt cga gtc cca gac   963
117 Thr Gly Thr Phe Asp Thr Val Leu Trp Ala Ile Gly Arg Val Pro Asp
118             305                 310                 315
120 acc aga agt ctg aat ttg gag aag gct ggg gta gat act agc ccc gac  1011
121 Thr Arg Ser Leu Asn Leu Glu Lys Ala Gly Val Asp Thr Ser Pro Asp
122     320                 325                 330
124 act cag aag atc ctg gtg gac tcc cgg gaa gcc acc tct gtg ccc cac  1059
125 Thr Gln Lys Ile Leu Val Asp Ser Arg Glu Ala Thr Ser Val Pro His
126 335                 340                 345                 350
128 atc tac gcc att ggt gac gtg gtg gag ggg cgg cct gag ctg aca ccc  1107
129 Ile Tyr Ala Ile Gly Asp Val Val Glu Gly Arg Pro Glu Leu Thr Pro
130                 355                 360                 365
132 aca gcg atc atg gcc ggg agg ctc ctg gtg cag cgg ctc ttc ggc ggg  1155
133 Thr Ala Ile Met Ala Gly Arg Leu Leu Val Gln Arg Leu Phe Gly Gly
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Input Set : A:\55871965.app
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134                 370                 375                 380
136 tcc tca gat ctg atg gac tac gac aat gtt ccc acg acc gtc ttc acc   1203
137 Ser Ser Asp Leu Met Asp Tyr Asp Asn Val Pro Thr Thr Val Phe Thr
138         385                 390                 395
140 cca ctg gag tat ggc tgt gtg ggg ctg tcc gag gag gag gca gtg gct   1251
141 Pro Leu Glu Tyr Gly Cys Val Gly Leu Ser Glu Glu Glu Ala Val Ala
142     400                 405                 410
144 cgc cac ggg cag gag cat gtt gag gtc tat cac gcc cat tat aaa cca   1299
145 Arg His Gly Gln Glu His Val Glu Val Tyr His Ala His Tyr Lys Pro
146 415                 420                 425                 430
148 ctg gag ttc acg gtg gct gga cga gat gca tcc cag tgt tat gta aag   1347
149 Leu Glu Phe Thr Val Ala Gly Arg Asp Ala Ser Gln Cys Tyr Val Lys
150                 435                 440                 445
152 atg gtg tgc ctg agg gag ccc cca cag ctg gtg ctg ggc ctg cat ttc   1395
153 Met Val Cys Leu Arg Glu Pro Pro Gln Leu Val Leu Gly Leu His Phe
154         450                 455                 460
156 ctt ggc ccc aac gca ggc gaa gtt act caa gga ttt gct ctg ggg atc   1443
157 Leu Gly Pro Asn Ala Gly Glu Val Thr Gln Gly Phe Ala Leu Gly Ile
158         465                 470                 475
160 aag tgt ggg gct tcc tat gcg cag gtg atg cgg acc gtg ggt atc cat   1491
161 Lys Cys Gly Ala Ser Tyr Ala Gln Val Met Arg Thr Val Gly Ile His
162     480                 485                 490
164 ccc aca tgc tct gag gag gta gtc aag ctg cgc atc tcc aag cgc tca   1539
165 Pro Thr Cys Ser Glu Glu Val Val Lys Leu Arg Ile Ser Lys Arg Ser
166 495                 500                 505                 510
168 ggc ctg gac ccc acg gtg aca ggc tgc tga ggg taagcgccat ccctgcaggc   1592
169 Gly Leu Asp Pro Thr Val Thr Gly Cys Xaa Gly
170                 515                 520
172 cagggcacac ggtgcgcccg ccgccagctc ctcggaggcc agacccagga tggctgcagg   1652
174 ccaggtttgg ggggcctcaa ccctctcctg gagcgcctgt gagatggtca gcgtggagcg   1712
176 caagtgctgg acgggtggcc cgtgtgcccc acagggatgg ctcaggggac tgtccacctc   1772
178 acccctgcac ctttcagcct ttgccgccgg gcaccccccc caggctcctg gtgccggatg   1832
180 atgacgacct gggtggaaac ctaccctgtg ggcacccatg tccgagcccc ctggcatttc   1892
182 tgcaatgcaa ataaagaggg tacttttct gaagtgtgta aaaaaaaaa aaaaaaaaa   1952
184 aaaaaaa                                                         1959
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187 <210> SEQ ID NO: 2
188 <211> LENGTH: 521
189 <212> TYPE: PRT
190 <213> ORGANISM: Homo sapiens
192 <220> FEATURE:
193 <221> NAME/KEY: MOD_RES
194 <222> LOCATION: (520)
195 <223> OTHER INFORMATION: Selenocysteine
197 <400> SEQUENCE: 2

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201 Gln Ala Val Ala Gly Gly Val Arg Gly Ala Ala Arg Gly Ala Ala Ala
202             20                  25                  30
204 Gly Gln Arg Asp Tyr Asp Leu Leu Val Val Gly Gly Gly Ser Gly Gly
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DATE: 11/14/2001
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Input Set : A:\55871965.app
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205           35                    40                    45
207 Leu Ala Cys Ala Lys Glu Ala Ala Gln Leu Gly Arg Lys Val Ala Val
208     50                  55                  60
210 Val Asp Tyr Val Glu Pro Ser Pro Gln Gly Thr Arg Trp Gly Leu Gly
211  65                  70                  75                  80
213 Gly Thr Cys Val Asn Val Gly Cys Ile Pro Lys Lys Leu Met His Gln
214                 85                  90                  95
216 Ala Ala Leu Leu Gly Gly Leu Ile Gln Asp Ala Pro Asn Tyr Gly Trp
217             100                 105                 110
219 Glu Val Ala Gln Pro Val Pro His Asp Trp Arg Lys Met Ala Glu Ala
220         115                 120                 125
222 Val Gln Asn His Val Lys Ser Leu Asn Trp Gly His Arg Val Gln Leu
223     130                 135                 140
225 Gln Asp Arg Lys Val Lys Tyr Phe Asn Ile Lys Ala Ser Phe Val Asp
226 145                 150                 155                 160
228 Glu His Thr Val Cys Gly Val Ala Lys Gly Gly Lys Glu Ile Leu Leu
229             165                 170                 175
231 Ser Ala Asp His Ile Ile Ile Ala Thr Gly Gly Arg Pro Arg Tyr Pro
232             180                 185                 190
234 Thr His Ile Glu Gly Ala Leu Glu Tyr Gly Ile Thr Ser Asp Asp Ile
235         195                 200                 205
237 Phe Trp Leu Lys Glu Ser Pro Gly Lys Thr Leu Val Val Gly Ala Ser
238     210                 215                 220
240 Tyr Val Ala Leu Glu Cys Ala Gly Phe Leu Thr Gly Ile Gly Leu Asp
241 225                 230                 235                 240
243 Thr Thr Ile Met Met Arg Ser Ile Pro Leu Arg Gly Phe Asp Gln Gln
244             245                 250                 255
246 Met Ser Ser Met Val Ile Glu His Met Ala Ser His Gly Thr Arg Phe
247             260                 265                 270
249 Leu Arg Gly Cys Ala Pro Ser Arg Val Arg Arg Leu Pro Asp Gly Gln
250         275                 280                 285
252 Leu Gln Val Thr Trp Glu Asp Ser Thr Thr Gly Lys Glu Asp Thr Gly
253     290                 295                 300
255 Thr Phe Asp Thr Val Leu Trp Ala Ile Gly Arg Val Pro Asp Thr Arg
256 305                 310                 315                 320
258 Ser Leu Asn Leu Glu Lys Ala Gly Val Asp Thr Ser Pro Asp Thr Gln
259             325                 330                 335
261 Lys Ile Leu Val Asp Ser Arg Glu Ala Thr Ser Val Pro His Ile Tyr
262         340                 345                 350
264 Ala Ile Gly Asp Val Val Glu Gly Arg Pro Glu Leu Thr Pro Thr Ala
265         355                 360                 365
267 Ile Met Ala Gly Arg Leu Leu Val Gln Arg Leu Phe Gly Gly Ser Ser
268     370                 375                 380
270 Asp Leu Met Asp Tyr Asp Asn Val Pro Thr Thr Val Phe Thr Pro Leu
271 385                 390                 395                 400
273 Glu Tyr Gly Cys Val Gly Leu Ser Glu Glu Glu Ala Val Ala Arg His
274             405                 410                 415
276 Gly Gln Glu His Val Glu Val Tyr His Ala His Tyr Lys Pro Leu Glu
277             420                 425                 430
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PATENT APPLICATION: US/09/830,706

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279 Phe Thr Val Ala Gly Arg Asp Ala Ser Gln Cys Tyr Val Lys Met Val
280         435                 440                 445
282 Cys Leu Arg Glu Pro Pro Gln Leu Val Leu Gly Leu His Phe Leu Gly
283     450                 455                 460
285 Pro Asn Ala Gly Glu Val Thr Gln Gly Phe Ala Leu Gly Ile Lys Cys
286 465                 470                 475                 480
288 Gly Ala Ser Tyr Ala Gln Val Met Arg Thr Val Gly Ile His Pro Thr
289                 485                 490                 495
291 Cys Ser Glu Glu Val Val Lys Leu Arg Ile Ser Lys Arg Ser Gly Leu
292             500                 505                 510
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295         515                 520
298 <210> SEQ ID NO: 3
299 <211> LENGTH: 2056
300 <212> TYPE: DNA
301 <213> ORGANISM: Homo sapiens
303 <220> FEATURE:
304 <221> NAME/KEY: CDS
305 <222> LOCATION: (188)..(1669)
307 <220> FEATURE:
308 <221> NAME/KEY: MOD_RES
309 <222> LOCATION: (493)
310 <223> OTHER INFORMATION: Selenocysteine
312 <400> SEQUENCE: 3
313 gtcccggacc tcaggcccag ttcagtgtac ttcccctctc tacttcctcc ctccagtccc 60
315 ttctccatcc ctcccttttt tggctgcccc ttgcctgcct tcctcgccag tagcttgcag 120
317 agtagacacg atgacacctt ttgcaggcta aaaaggctga gagtggcact atgtgcagtg 180
319 agccacc atg gag gac caa gca ggt cag cgg gac tat gat ctc ctg gtg 229
320         Met Glu Asp Gln Ala Gly Gln Arg Asp Tyr Asp Leu Leu Val
321           1               5                   10
323 gtc ggc ggg gga tct ggt ggc ctg gct tgt gcc aag gag gcc gcc cag 277
324 Val Gly Gly Gly Ser Gly Gly Leu Ala Cys Ala Lys Glu Ala Ala Gln
325  15                 20                  25                  30
327 ctg gga agg aag gtg gcc gtg gtg gac tac gtg gaa cct tct ccc caa 325
328 Leu Gly Arg Lys Val Ala Val Val Asp Tyr Val Glu Pro Ser Pro Gln
329                 35                  40                  45
331 ggc acc cgg tgg ggc ctc ggc ggc acc tgc gtc aac gtg ggc tgc atc 373
332 Gly Thr Arg Trp Gly Leu Gly Gly Thr Cys Val Asn Val Gly Cys Ile
333                 50                  55                  60
335 ccc aag aag ctg atg cac cag gcg gca ctg ctg gga ggc ctg atc caa 421
336 Pro Lys Lys Leu Met His Gln Ala Ala Leu Leu Gly Gly Leu Ile Gln
337             65                  70                  75
339 gat gcc ccc aac tat ggc tgg gag gtg gcc cag ccc gtg ccg cat gac 469
340 Asp Ala Pro Asn Tyr Gly Trp Glu Val Ala Gln Pro Val Pro His Asp
341         80                  85                  90
343 tgg agg aag atg gca gaa gct gtt caa aat cac gtg aaa tcc ttg aac 517
344 Trp Arg Lys Met Ala Glu Ala Val Gln Asn His Val Lys Ser Leu Asn
345  95                 100                 105                 110
347 tgg ggc cac cgt gtc cag ctt cag gac aga aaa gtc aag tac ttt aac 565
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VERIFICATION SUMMARY
PATENT APPLICATION: **US/09/830,706**

DATE: 11/14/2001
TIME: 14:12:31

Input Set : **A:\55871965.app**
Output Set: **N:\CRF3\11142001\I830706.raw**

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L:169  M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:294  M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2
L:440  M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:559  M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4
L:2002 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:37
L:3285 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:38
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